



## SEQUENCE LISTING

<110> Guerry, Patricia  
Trust, Trevor J  
Burg, Edward  
Lee, Lanfong

<120> A Recombinant Polypeptide for use in the Manufacture of Vaccines  
against Campylobacter Induced Diarrhea and to Reduce Colonization

<130> 78560

<140> 09/439,311

<141> 1999-11-12

<150> US 60/108,114

<151> 1998-11-12

<160> 6

<170> Apple Macintosh Microsoft Word 6.0

<210> 1

<211> 999

<212> DNA

<213> Campylobacter coli

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gcttcaggga tggcgatagc agatagttta agatctcagg caaatacttt gggtcaggct 180  
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caacttaaaa tcttagatac catcaagact aaagcgactc aagctgctca agatgggtcaa 300  
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aatatcgcaa ataccacttc atttaattggc aaacaacttt taagtgggtg ttttaccat 420  
caagaattcc aaatcggttc aagttcaaat caaactatta aagcaagtat aggagcaact 480  
cagtcttcta aaatcggtgt aacaagattt gaaacagggt caciaagttt tcttcaggc 540  
actgtaggac ttactattaa aaactacaac ggtatcgaag attttaaatt tgatagtgt 600  
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RECEIVED

JAN 08 2002

OFFICE OF PETITIONS

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actggtgttc aagcctctaa agatgaaaat ggtaaacttg ttcttacttc ggccgatggg 900
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Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala Ser Gly Met Ala
          35          40          45
Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr Leu Gly Gln Ala
          50          55          60
Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu Gln Thr Ala Asp
          65          70          75
Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp Thr Ile Lys Thr
          80          85          90
Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser Leu Lys Thr Arg
          95          100          105
Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met Glu Glu Leu Asp
          110          115          120
Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys Gln Leu Leu Ser
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Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly Ser Ser Ser Asn
          140          145          150
Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln Ser Ser Lys Ile
          155          160          165
Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser Phe Ser Ser Gly
          170          175          180
Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly Ile Glu Asp Phe
          185          190          195
Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val Gly Thr Gly Leu
          200          205          210
Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala Asp Lys Thr Gly
          215          220          225
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Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile Asn Gly Val Val
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Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu Asn Gly Ser Leu  
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 Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr Gly Val Gln Ala  
 275 280 285  
 Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr Ser Ala Asp Gly  
 290 295 300  
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 Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala  
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 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr  
 50 55 60  
 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu  
 65 70 75  
 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp  
 80 85 90  
 Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser  
 95 100 105  
 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met  
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 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys  
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 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly  
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 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln  
 155 160 165  
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 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly  
 185 190 195  
 Ile Glu Asp Phe Lys Phe Asp Ser Val Val Ile Ser Thr Ser Val  
 200 205 210  
 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala  
 215 220 225  
 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly  
 230 235 240  
 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile  
 245 250 255  
 Asn Gly Val Val Ile Gly Gln Ile Asn Tyr Asn Asp Gly Asp Asn  
 260 265 270  
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 275 280 285  
 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr  
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 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val  
 305 310 315  
 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu  
 320 325 330  
 Val Lys Asn Asp Gly Arg Asp Ile Asn Ile Ser Gly Thr Gly Leu  
 335 340 345  
 Ser Ala Ile Gly Met Gly Ala Thr Asp Met Ile Ser Gln Ser Ser  
 350 355 360  
 Val Ser Leu Arg Glu Ser Lys Gly Gln Ile Ser Ala Ala Asn Ala  
 365 370 375

Asp Ala Met Gly Phe Asn Ser Tyr Lys Gly Gly Gly Lys Phe Val  
 380 385 390  
 Phe Thr Gln Asn Val Ser Ser Ile Ser Ala Phe Met Ser Ala Gln  
 395 400 405  
 Gly Ser Gly Phe Ser Arg Gly Ser Gly Phe Ser Val Gly Ser Gly  
 410 415 420  
 Lys Asn Leu Ser Val Gly Leu Ser Gln Gly Ile Gln Ile Ile Ser  
 425 430 435  
 Ser Ala Ala Ser Met Ser Asn Thr Tyr Val Val Ser Ala Gly Ser  
 440 445 450  
 Gly Phe Ser Ser Gly Ser Gly Asn Ser Gln Phe Ala Ala Leu Lys  
 455 460 465  
 Thr Thr Ala Ala Asn Thr Thr Asp Glu Thr Ala gly Val Thr Thr  
 470 475 480  
 Leu Lys Gly Ala Met Ala Val Met Asp Ile Ala Glu Thr Ala Ile  
 485 490 495  
 Thr Asn Leu Asp Gln Ile Arg Ala Asp Ile Gly Ser Ile Gln Asn  
 500 505 510  
 Gln Val Thr Ser Thr Ile Asn Asn Ile Thr Val Thr Gln Val Asn  
 515 520 525  
 Val Lys Ala Ala Glu Ser Gln Ile Arg Asp Val Asp Phe Ala Ser  
 530 535 540  
 Glu Ser Ala Asn Tyr Ser Lys Ala Asn Ile Leu Ala Gln Ser Gly  
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<212> PRT

<213> Campylobacter coli VC167 T2

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 Arg Leu Ser Ser Gly Leu Arg Ile Asn Ser Ala Ala Asp Asp Ala  
 35 40 45  
 Ser Gly Met Ala Ile Ala Asp Ser Leu Arg Ser Gln Ala Asn Thr  
 50 55 60  
 Leu Gly Gln Ala Ile Ser Asn Gly Asn Asp Ala Leu Gly Ile Leu  
 65 70 75  
 Gln Thr Ala Asp Lys Ala Met Asp Glu Gln Leu Lys Ile Leu Asp  
 80 85 90

Thr Ile Lys Thr Lys Ala Thr Gln Ala Ala Gln Asp Gly Gln Ser  
 95 100 105  
 Leu Lys Thr Arg Thr Met Leu Gln Ala Asp Ile Asn Arg Leu Met  
 110 115 120  
 Glu Glu Leu Asp Asn Ile Ala Asn Thr Thr Ser Phe Asn Gly Lys  
 125 130 135  
 Gln Leu Leu Ser Gly Gly Phe Thr Asn Gln Glu Phe Gln Ile Gly  
 140 145 150  
 Ser Ser Ser Asn Gln Thr Ile Lys Ala Ser Ile Gly Ala Thr Gln  
 155 160 165  
 Ser Ser Lys Ile Gly Val Thr Arg Phe Glu Thr Gly Ser Gln Ser  
 170 175 180  
 Phe Ser Ser Gly Thr Val Gly Leu Thr Ile Lys Asn Tyr Asn Gly  
 185 190 195  
 Ile Glu Asp Phe Lys Phe Gln Ser Val Val Ile Ser Thr Ser Val  
 200 205 210  
 Gly Thr Gly Leu Gly Ala Leu Ala Glu Glu Ile Asn Arg Asn Ala  
 215 220 225  
 Asp Lys Thr Gly Ile Arg Ala Thr Phe Asp Val Lys Ser Val Gly  
 230 235 240  
 Ala Tyr Ala Ile Lys Ala Gly Asn Thr Ser Gln Asp Phe Ala Ile  
 245 250 255  
 Asn Gly Val Val Ile Gly Lys Val Asp Tyr Ser Asp Gly Asp Glu  
 260 265 270  
 Asn Gly Ser Leu Ile Ser Ala Ile Asn Ala Val Lys Asp Thr Thr  
 275 280 285  
 Gly Val Gln Ala Ser Lys Asp Glu Asn Gly Lys Leu Val Leu Thr  
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 Ser Ala Asp Gly Arg Gly Ile Lys Ile Thr Gly Ser Ile Gly Val  
 305 310 315  
 Gly Ala Gly Ile Leu His Thr Glu Asn Tyr Gly Arg Leu Ser Leu  
 320 325 330  
 Val Lys Asn Asp Gly Arg Asp Ile Asn Ile Ser Gly Thr Gly Leu  
 335 340 345  
 Ser Ala Ile Gly Met Gly Ala Thr Asp Met Ile Ser Gln Ser Ser  
 350 355 360  
 Val Ser Leu Arg Glu Ser Lys Gly Gln Ile Ser Ala Ala Asn Ala  
 365 370 375  
 Asp Ala Met Gly Phe Asn Ala Tyr Asn Gly Gly Gly Ala Lys Gln  
 380 385 390  
 Ile Ile Phe Ala Ser Ser Ile Ala Gly Phe Met Ser Gln Ala Gly  
 395 400 405  
 Ser Gly Phe Ser Ala Gly Ser Gly Phe Ser Val Gly Ser Gly Lys  
 410 415 420  
 Asn Tyr Ser Ala Ile Leu Ser Ala Ser Ile Gln Ile Val Ser Ser  
 425 430 435  
 Ala Arg Ser Ile Ser Ser Thr Tyr Val Val Ser Thr Gly Ser Gly  
 440 445 450  
 Phe Ser Ala Gly Ser Gly Asn Ser Gln Phe Ala Ala Leu Arg Ile  
 455 460 465  
 Ser Thr Val Ser Ala His Asp Glu Thr Ala Gly Val Thr Thr Leu  
 470 475 480  
 Lys Gly Ala Met Ala Val Met Asp Ile Ala Glu Thr Ala Ile Thr  
 485 490 495

Asn	Leu	Asp	Gln	Ile	Arg	Ala	Asp	Ile	Gly	Ser	Val	Gln	Asn	Gln
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Ile	Thr	Ser	Thr	Ile	Asn	Asn	Ile	Thr	Val	Thr	Gln	Val	Asn	Val
				515					520					525
Lys	Ser	Ala	Glu	Ser	Gln	Ile	Arg	Asp	Val	Asp	Phe	Ala	Ser	Glu
				530					535					540
Ser	Ala	Asn	Tyr	Ser	Lys	Ala	Asn	Ile	Leu	Ala	Gln	Ser	Gly	Ser
				545					550					555
Tyr	Ala	Met	Ala	Gln	Ala	Asn	Ser	Ser	Gln	Gln	Asn	Val	Leu	Arg
				560					565					570
Leu	Leu	Gln												

ap

